

GenCore version 5.1.6
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OK nucleic - nucleic search, using sw model

Run on: August 4, 2004, 06:01:54 ; Search time 36.1446 Seconds

(without alignments)
307.073 Million cell updates/sec

Title: US-09-940-860-1

Sequence: 1.gcaaacagattagatcccc 20

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 27747546 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

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5: /cgn2_6/ptodata/2/ina/PTCUTS.COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfiles.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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2	20	100.0	195 1 US-08-227-475-7	Sequence 7, Appli
3	20	100.0	279 4 US-09-107-532A-3170	Sequence 3170, Ap
4	20	100.0	279 4 US-09-107-532A-3171	Sequence 3171, Ap
5	20	100.0	538 3 US-08-979-566-3	Sequence 3, Appli
6	20	100.0	538 4 US-09-577-640-3	Sequence 3, Appli
7	20	100.0	571 3 US-09-328-111-755	Sequence 755, App
8	20	100.0	619 3 US-08-953-171-2	Sequence 2, Appli
9	20	100.0	624 3 US-09-328-111-728	Sequence 728, App
10	20	100.0	660 1 US-08-114-695A-5	Sequence 5, Appli
11	20	100.0	665 3 US-09-328-111-476	Sequence 476, App
12	20	100.0	672 3 US-09-328-111-450	Sequence 450, App
13	20	100.0	851 1 US-07-898-905-1	Sequence 1, Appli
14	20	100.0	851 1 US-07-898-905-2	Sequence 2, Appli
15	20	100.0	851 1 US-07-898-905-3	Sequence 3, Appli
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19	20	100.0	876 2 US-08-642-229A-4	Sequence 4, Appli
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21	20	100.0	882 2 US-07-923-871C-13	Sequence 13, Appli
22	20	100.0	1208 3 US-09-187-946-1	Sequence 1, Appli
23	20	100.0	1325 2 US-08-632-470-50	Sequence 50, Appli
24	20	100.0	1336 2 US-08-437-013-3	Sequence 3, Appli
25	20	100.0	1366 4 US-09-275-506A-3	Sequence 4, Appli
26	20	100.0	1366 4 US-09-191-099-4	Sequence 4, Appli
27	20	100.0	1385 4 US-09-735-567-1	Sequence 1, Appli

28	20	100.0	1396 3 US-08-953-171-6	Sequence 6, Appli
29	20	100.0	1400 4 US-09-375-932A-5	Sequence 5, Appli
30	20	100.0	1405 3 US-09-191-099-5	Sequence 5, Appli
31	20	100.0	1407 3 US-09-193-377B-2	Sequence 2, Appli
32	20	100.0	1407 4 US-09-517-744B-1	Sequence 1, Appli
33	20	100.0	1408 2 US-08-632-470-40	Sequence 40, Appli
34	20	100.0	1413 3 US-09-191-099-1	Sequence 1, Appli
35	20	100.0	1414 3 US-09-191-099-6	Sequence 6, Appli
36	20	100.0	1415 2 US-08-632-470-52	Sequence 52, Appli
37	20	100.0	1415 3 US-09-193-377B-9	Sequence 9, Appli
38	20	100.0	1417 4 US-09-565-063-2	Sequence 2, Appli
39	20	100.0	1419 4 US-08-266-414-1	Sequence 1, Appli
40	20	100.0	1420 1 US-09-193-377B-4	Sequence 4, Appli
41	20	100.0	1420 3 US-09-193-377B-7	Sequence 7, Appli
42	20	100.0	1426 3 US-08-632-470-27	Sequence 27, Appli
43	20	100.0	1427 2 US-08-632-470-27	Sequence 27, Appli
44	20	100.0	1428 3 US-09-193-377B-1	Sequence 1, Appli
45	20	100.0	1429 3 US-09-193-377B-8	Sequence 8, Appli

ALIGNMENTS

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RESULT 1
US-09-073-465-9
; Sequence 9, Application US/09073465
; Patent No. 6054278
; GENERAL INFORMATION:
; APPLICANT: DODGE, Deborah E
; APPLICANT: SMITH, Doug
; TITLE OF INVENTION: RIBOSOMAL RNA GENE POLYMORPHISM BASED MICROORGANISM
; FILE REFERENCE: 4343 US
; CURRENT APPLICATION NUMBER: US/09/073,465
; CURRENT FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentm Ver. 2.1
; SEQ ID NO 9
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Bacterial
; US-09-073-465-9

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Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCAAAACGAGTTAGATACCC 20
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Db       2 GCAAAACGAGTTAGATACCC 21

RESULT 2
US-08-227-475-7/c
; Sequence 7, Application US/08227475
; Patent No. 5571674
; GENERAL INFORMATION:
; APPLICANT: Hoshina, Sadayori
; APPLICANT: Weinstein, I. Bernard
; TITLE OF INVENTION: DNA Oligomers For Use In Detection Of
; TITLE OF INVENTION: Microorganisms And Methods Of Using Such DNA
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: COOPER & DUNHAM
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OW nucleic - nucleic search, using sw model

Run on: August 4, 2004, 06:01:54 ; Search time 36.1446 Seconds

(without alignments)
307.073 Million cell updates/sec

Title: US-09-940-860-2
Perfect score: 20
Sequence: 1 ggaggaagcgagagatgacg 20

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 682709 segs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents NA: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	20	100.0	2751	3 US-09-052-333A-6	Sequence 6, Appl
3	20	100.0	2762	3 US-09-052-333A-37	Sequence 37, Appl
4	20	100.0	1230025	4 US-09-198-452A-1	Sequence 1, Appl
5	16	80.0	420	4 US-09-252-991A-11029	Sequence 11029, A
6	16	80.0	1107	4 US-09-252-991A-1336	Sequence 1336, A
7	16	80.0	1179	4 US-09-252-991A-13193	Sequence 13193, A
8	16	80.0	1308	4 US-09-252-991A-12614	Sequence 12614, A
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10	16	80.0	1974	4 US-09-252-991A-11111	Sequence 11111, A
11	16	80.0	2283	4 US-09-252-991A-10956	Sequence 10956, A
12	15	75.0	191	4 US-09-621-976-8573	Sequence 8573, Ap
13	15	75.0	752	3 US-08-818-1112-2	Sequence 2, Appl
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17	15	75.0	752	4 US-09-072-567-2	Sequence 2, Appl
18	15	75.0	889	4 US-09-050-739-5	Sequence 5, Appl
19	15	75.0	1245	4 US-09-252-991A-6286	Sequence 6286, Ap
20	15	75.0	1980	4 US-09-252-991A-6369	Sequence 6369, Ap
21	15	75.0	2499	4 US-09-252-991A-6182	Sequence 6182, Ap
22	15	75.0	4403765	3 US-09-103-840A-2	Sequence 2, Appl
23	15	75.0	4411529	3 US-09-103-840A-1	Sequence 1, Appl
24	14	70.0	396	4 US-09-252-991A-6707	Sequence 6707, Ap
25	14	70.0	541	4 US-09-743-207-13	Sequence 13, Appl
26	14	70.0	738	4 US-09-252-991A-2237	Sequence 2237, Ap
27	14	70.0	885	4 US-09-252-991A-10382	Sequence 10382, A

C 28	14	70.0	1206	4 US-09-489-039A-4798	Sequence 4798, Ap
C 29	14	70.0	1260	4 US-09-252-991A-6674	Sequence 6674, Ap
C 30	14	70.0	1717	4 US-09-673-395A-11	Sequence 11, Appl
C 31	14	70.0	1734	4 US-09-252-991A-2607	Sequence 2607, Ap
C 32	14	70.0	2016	4 US-09-252-991A-2445	Sequence 2445, Ap
C 33	14	70.0	2141	4 US-09-620-312D-635	Sequence 635, Ap
C 34	14	70.0	2163	4 US-09-252-991A-6641	Sequence 6641, Ap
C 35	14	70.0	2169	4 US-09-735-934A-1	Sequence 10268, A
C 36	14	70.0	2637	4 US-09-735-934A-1	Sequence 1, Appl
C 37	14	70.0	2637	4 US-10-060-332-1	Sequence 1, Appl
C 38	14	70.0	3437	4 US-08-450-962-3	Sequence 3, Appl
C 39	14	70.0	3437	4 US-08-848-631-3	Sequence 3, Appl
C 40	14	70.0	8906	2 US-08-826-267-1	Sequence 1, Appl
C 41	14	70.0	17138	3 US-09-813-819-3	Sequence 3, Appl
C 42	14	70.0	17138	4 US-09-920-048-3	Sequence 3, Appl
C 43	14	70.0	43950	4 US-09-735-934A-3	Sequence 3, Appl
C 44	14	70.0	43950	4 US-10-060-332-3	Sequence 3, Appl
C 45	13	65.0	20	4 US-09-302-681-91	Sequence 91, Appl

ALIGNMENTS

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RESULT 1
US-09-726-774-11
Sequence 11, Application US/09726774
Patent No. 6677153
GENERAL INFORMATION:
APPLICANT: Iversen, Patrick L.
TITLE OF INVENTION: Antisense Antibacterial Method and
FILE REFERENCE: 0450-0032.30
CURRENT APPLICATION NUMBER: US/09/726,774
PRIOR FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: US 60/168,150
NUMBER OF SEQ ID NOS: 139
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 1548
TYPE: DNA
ORGANISM: Chlamydia trachomatis
US-09-726-774-11

Query Match      100.0%; Score 20; DB 4; Length 1548;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 GGAGGAGGCGAGGATGACG 20
Db      1179 GGAGGAGGCGAGGATGACG 1198

RESULT 2
US-09-052-333A-6
Sequence 6, Application US/09052333A
Patent No. 6261769
GENERAL INFORMATION:
APPLICANT: Everett, Karin D.E.
APPLICANT: Andersen, Arthur A.
TITLE OF INVENTION: Intergenic Spacer Target Sequence for
Patent No. 6261769
TITLE OF INVENTION: Detecting and Distinguishing Chlamydial Strains
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSER: Curtis P. Ribando
STREET: 1815 N. University Street
CITY: Peoria
STATE: IL
COUNTRY: US
ZIP: 61604
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,333A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ribando, Curtis P.
REGISTRATION NUMBER: 27,976
REFERENCE/DOCKET NUMBER: 0211.97
TELECOMMUNICATION INFORMATION:
TELEPHONE: 309/681-6513
TELEFAX: 309/681-6688
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2751 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: rRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Chlamydia psittaci
STRAIN: NJ1
FEATURE:
NAME/KEY: rRNA
LOCATION: 1..564
OTHER INFORMATION: /note= "16S rRNA"
FEATURE:
NAME/KEY: misc_RNA
LOCATION: 565..788
OTHER INFORMATION: /note= "intergenic spacer"
FEATURE:
NAME/KEY: rRNA
LOCATION: 789..1409
OTHER INFORMATION: /note= "Domain I of the 23S rRNA"
FEATURE:
NAME/KEY: rRNA
LOCATION: 789..2751
OTHER INFORMATION: /note= "23S rRNA"
FEATURE:
NAME/KEY: misc_RNA
LOCATION: 346..881
OTHER INFORMATION: /note= "Region A - Region of the
OTHER INFORMATION: Intergenic Spacer"
FEATURE:
NAME/KEY: rRNA
LOCATION: 1303..1432
OTHER INFORMATION: /note= "Region B - The 3' End of
OTHER INFORMATION: Domain I in the 23S rRNA"
US-09-052-333A-6

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGAGGCGGAGGATGACG 20
DB 193 GGAGGAGGCGGAGGATGACG 212

RESULT 3
US-09-052-333A-37
Sequence 37, Application US/09052333A
Patent No. 6261769
GENERAL INFORMATION:
APPLICANT: Everett, Karin D.E.
APPLICANT: Andersen, Arthur A.
TITLE OF INVENTION: Intergenic Spacer Target Sequence for
OF INVENTION: Detecting and Distinguishing Chlamydial Strains
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NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis P. Ribando
STREET: 1815 N. University Street
CITY: Peoria
STATE: IL
COUNTRY: US
ZIP: 61604
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,333A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ribando, Curtis P.
REGISTRATION NUMBER: 27,976
REFERENCE/DOCKET NUMBER: 0211.97
TELECOMMUNICATION INFORMATION:
TELEPHONE: 309/681-6513
TELEFAX: 309/681-6688
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 2762 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: rRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Chlamydia trachomatis
STRAIN: R22
FEATURE:
NAME/KEY: rRNA
LOCATION: 1..564
OTHER INFORMATION: /note= "16S rRNA"
FEATURE:
NAME/KEY: misc_RNA
LOCATION: 565..802
OTHER INFORMATION: /note= "intergenic spacer"
FEATURE:
NAME/KEY: rRNA
LOCATION: 803..1424
OTHER INFORMATION: /note= "Domain I of the 23S rRNA"
FEATURE:
NAME/KEY: rRNA
LOCATION: 803..2762
OTHER INFORMATION: /note= "23S rRNA"
FEATURE:
NAME/KEY: misc_RNA
LOCATION: 346..895
OTHER INFORMATION: /note= "Region A - Region of the
OTHER INFORMATION: Intergenic Spacer"
FEATURE:
NAME/KEY: rRNA
LOCATION: 1320..1447
OTHER INFORMATION: /note= "Region B - The 3' End of
OTHER INFORMATION: Domain I in the 23S rRNA"
US-09-052-333A-37

Query Match 100.0%; Score 20; DB 3; Length 2762;
Best Local Similarity 100.0%; Pred. NO. 0.015;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 193 GGAGGAGGCGGAGGATGACG 212
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ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/01574
FILING DATE: 19910507
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 489,676
FILING DATE: 07-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Kaster, Kevin R.
REGISTRATION NUMBER: 32,704
REFERENCE/DOCKET NUMBER: 2536.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 420-3444
TELEFAX: (415) 658-5239
TELEX: 4992659
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 505 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: unsure
LOCATION: complement (35..36)
FEATURE:
NAME/KEY: unsure
LOCATION: complement (41)
FEATURE:
NAME/KEY: unsure
LOCATION: complement (67)
FEATURE:
NAME/KEY: unsure
LOCATION: complement (164..165)
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PCT-US91-01574-1

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Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 396 ACAGAGCCGAGACGTATTCA 375

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US-09-052-333A-26/c
Sequence 26, Application US/09052333A
Patent No. 6261769
GENERAL INFORMATION:
APPLICANT: Everett, Karin D.E.
APPLICANT: Andersen, Arthur A.
TITLE OF INVENTION: Intergenic Spacer Target Sequence for
Patent No. 6261769
TITLE OF INVENTION: Detecting and Distinguishing Chlamydial Strains
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis P. Ribando
STREET: 1815 N. University Street

CITY: Peoria
STATE: IL
COUNTRY: US
ZIP: 61604
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,333A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ribando, Curtis P.
REGISTRATION NUMBER: 27,976
REFERENCE/DOCKET NUMBER: 0211.97
TELECOMMUNICATION INFORMATION:
TELEPHONE: 309/681-6513
TELEFAX: 309/681-6688
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1284 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: rRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Chlamydia pneumoniae
STRAIN: CWL-029
FEATURE:
NAME/KEY: rRNA
LOCATION: 1..221
OTHER INFORMATION: /note= "16S rRNA"
FEATURE:
NAME/KEY: misc RNA
LOCATION: 222..444
OTHER INFORMATION: /note= "intergenic spacer"
FEATURE:
NAME/KEY: rRNA
LOCATION: 445..1063
OTHER INFORMATION: /note= "Domain I of the 23S rRNA"
FEATURE:
NAME/KEY: rRNA
LOCATION: 445..1284
OTHER INFORMATION: /note= "23S rRNA"
FEATURE:
NAME/KEY: misc RNA
LOCATION: 1..537
OTHER INFORMATION: /note= "Region A - Region of the
OTHER INFORMATION: Intergenic Spacer"
FEATURE:
NAME/KEY: rRNA
LOCATION: 959..1086
OTHER INFORMATION: /note= "Region B - The 3' End of
OTHER INFORMATION: Domain I in the 23S rRNA"
US-09-052-333A-26

Query Match 100.0%; Score 22; DB 3; Length 1284;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 67 ACAGAGCCGAGACGTATTCA 46

RESULT 6
US-09-052-333A-27/c
Sequence 27, Application US/09052333A
Patent No. 6261769

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 04:03:11 ; Search time 919.446 Seconds

(without alignments)
989,948 Million cell updates/sec

Title: US-09-940-860-4

Sequence: 1 gtcgcagcagcagcggtactata 21

Scoring table: OLIGO NUC

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Searched: 3470272 segs, 2167151695 residues

Word size: 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	410	1	AF128731
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6	21	100.0	500	1	AF280951
7	21	100.0	508	1	AF193254
8	21	100.0	517	1	AF193029
9	21	100.0	525	1	AF193103
10	21	100.0	529	3	AF293558
11	21	100.0	534	8	AF442312
12	21	100.0	550	1	AF128705
13	21	100.0	552	8	AF442310
14	21	100.0	559	1	AF037640
15	21	100.0	564	1	AF193243
16	21	100.0	572	1	AF037568
17	21	100.0	575	1	AF037566
18	21	100.0	585	1	AF432842
19	21	100.0	600	8	AF442309
20	21	100.0	620	1	AF242747
21	21	100.0	620	1	AF242748
22	21	100.0	621	1	AF037626
23	21	100.0	648	3	AF293557
24	21	100.0	650	1	AF037620
25	21	100.0	670	1	AF193253
26	21	100.0	702	1	AF469392
27	21	100.0	756	1	AF245484
28	21	100.0	766	1	AF193246
29	21	100.0	771	1	AF469403
30	21	100.0	784	1	AF469398
31	21	100.0	796	1	AF245486
32	21	100.0	824	1	AF469407
33	21	100.0	935	3	PFAMTSST
34	21	100.0	939	3	AF040972
35	21	100.0	949	3	AF040974
36	21	100.0	956	1	GS16S759
37	21	100.0	961	3	AF040968
38	21	100.0	991	1	AF172925
39	21	100.0	991	1	AF172926
40	21	100.0	991	1	AF172927
41	21	100.0	995	1	AF172927
42	21	100.0	998	3	AF040976
43	21	100.0	1013	3	AF040975
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ALIGNMENTS

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RESULT 1
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LOCUS AF128731 410 bp DNA linear BCT 10-MAY-1999
DEFINITION Uncultured soil bacterium C065 16S ribosomal RNA, partial sequence.
ACCESSION AF128731
VERSION AF128731.1 GI:4761945
KEYWORDS
SOURCE
ORGANISM
Bacteria; environmental samples.
REFERENCE
1 (bases 1 to 410)
Dunbar,J., Takala,S., Barnes,S.M., Davis,J.A. and Kuske,C.R.
Levels of bacterial community diversity in four acid soils compared
by cultivation and 16S rRNA gene cloning in four acid soils compared
Appl. Environ. Microbiol. 65 (4), 1662-1669 (1999)
JOURNAL

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MEDLINE      99203125
PUBMED      10103265
REFERENCE    2 (bases 1 to 410)
AUTHORS      Dunbar,J., Takala,S., Barns,S.M., Davis,J.A. and Kuske,C.R.
TITLE        Direct Submission
JOURNAL      Submitted (15-FEB-1999) Environmental Molecular Biology, Life
              Sciences Division, Los Alamos National Laboratory, M888, Los
              Alamos, NM 87545, USA
FEATURES
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 GTGCCAGCAGCAGCGGTATA 21
171 GTGCCAGCAGCAGCGGTATA 191

RESULT 2
LOCUS      AF128692      420 bp      DNA      linear      BCT 10-MAY-1999
DEFINITION Uncultured soil bacterium S079 16S ribosomal RNA, partial sequence.
ACCESSION  AF128692
VERSION     AF128692.1 GI:4761906
KEYWORDS
SOURCE      uncultured soil bacterium S079
              Bacteria; environmental samples.
              1 (bases 1 to 420)
REFERENCE    Dunbar,J., Takala,S., Barns,S.M., Davis,J.A. and Kuske,C.R.
              Levels of bacterial community diversity in four arid soils compared
              by cultivation and 16S rRNA gene cloning
              Appl. Environ. Microbiol. 65 (4), 1662-1669 (1999)
JOURNAL      99203125
MEDLINE     10103265
PUBMED      2 (bases 1 to 420)
AUTHORS      Dunbar,J., Takala,S., Barns,S.M., Davis,J.A. and Kuske,C.R.
TITLE        Direct Submission
JOURNAL      Submitted (15-FEB-1999) Environmental Molecular Biology, Life
              Sciences Division, Los Alamos National Laboratory, M888, Los
              Alamos, NM 87545, USA
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Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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202 GTGCCAGCAGCAGCGGTATA 222

RESULT 3
LOCUS      AF247784      434 bp      DNA      linear      BCT 08-SEP-2000
DEFINITION Soil clone WDS 16S ribosomal RNA gene, partial sequence.
ACCESSION  AF247784
VERSION     AF247784.2 GI:9994208
KEYWORDS
SOURCE      soil clone WDS
              Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
              Sphingomonadaceae; environmental samples.
              1 (bases 1 to 434)
REFERENCE    Dejonghe,W., Goris,J., El Fantroussi,S., Hofte,M., De Vos,P.,
              Verstraete,W. and Top,E.M.
              Effect of dissemination of 2,4-dichlorophenoxyacetic acid (2,4-D)
              degradation plasmids on 2,4-D degradation and on bacterial
              community structure in two different soil horizons
              Appl. Environ. Microbiol. 66 (8), 3297-3304 (2000)
JOURNAL      10919784
MEDLINE     10919784
PUBMED      2 (bases 1 to 434)
AUTHORS      Dejonghe,W.L., Goris,J., El Fantroussi,S., Hofte,M., De Vos,P.,
              Verstraete,W. and Top,E.M.
TITLE        Direct Submission
JOURNAL      Submitted (23-MAR-2000) Faculty of Agricultural and Applied
              Biological Sciences, Gent University, Coupure Links 653, Gent 9000,
              Belgium
              3 (bases 1 to 434)
              Dejonghe,W.L., Goris,J., El Fantroussi,S., Hofte,M., De Vos,P.,
              Verstraete,W. and Top,E.M.
              Direct Submission
              Submitted (08-SEP-2000) Faculty of Agricultural and Applied
              Biological Sciences, Gent University, Coupure Links 653, Gent 9000,
              Belgium
              Sequence update by submitter
              On Sep 8, 2000 this sequence version replaced gi:9864056.
              Location/Qualifiers
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.8e+02;
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QY
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413 GTGCCAGCAGCAGCGGTATA 433

RESULT 4
LOCUS      AF128656      440 bp      DNA      linear      BCT 10-MAY-1999
DEFINITION Uncultured soil bacterium C0108 16S ribosomal RNA, partial
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ACCESSION  AF128656
VERSION     AF128656.1 GI:4761870
KEYWORDS
SOURCE      uncultured soil bacterium C0108
              Bacteria; environmental samples.
              1 (bases 1 to 440)
REFERENCE    Dunbar,J., Takala,S., Barns,S.M., Davis,J.A. and Kuske,C.R.
              Levels of bacterial community diversity in four arid soils compared
              by cultivation and 16S rRNA gene cloning
              Appl. Environ. Microbiol. 65 (4), 1662-1669 (1999)
JOURNAL      99203125
MEDLINE     10103265
PUBMED      2 (bases 1 to 440)
AUTHORS      Dunbar,J., Takala,S., Barns,S.M., Davis,J.A. and Kuske,C.R.
TITLE        Direct Submission
JOURNAL      Submitted (15-FEB-1999) Environmental Molecular Biology, Life

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